

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 10:30:26 ; Search time 25.2 Seconds

(without alignments)
34,318 Million cell updates/sec

Title: 09-403627-1
Perfect score: 45
Sequence: 1 avdlsflk 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 28318 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 788

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_71:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Length | DB ID | Description |
|------------|-------|--------------|----------|----------------------|
| 1 | 37.8 | 9 | 2 S07205 | litorin 2-Glu - Au |
| 2 | 37.8 | 9 | 2 S07204 | litorin I - Austro |
| 3 | 35.6 | 9 | 2 S07241 | litorin - Rohde's |
| 4 | 35.6 | 9 | 2 D48186 | ATPase RI subunit |
| 5 | 33.3 | 8 | 2 PC4131 | hypothetical prote |
| 6 | 33.3 | 9 | 2 JN0026 | sperm-activating p |
| 7 | 31.1 | 5 | 4 A58728 | serrawetlin W2 - S |
| 8 | 31.1 | 7 | 2 S20446 | elastase - Pseudom |
| 9 | 31.1 | 7 | 2 S78024 | ribosomal protein |
| 10 | 31.1 | 8 | 2 A42057 | fibroblast growth |
| 11 | 31.1 | 8 | 2 S66296 | Na+-transporting A |
| 12 | 31.1 | 9 | 2 B39841 | dextranucrase (EC |
| 13 | 31.1 | 9 | 2 A39841 | sucrose 3-glucosyl |
| 14 | 31.1 | 9 | 2 C57444 | neuropeptide Grb-A |
| 15 | 28.9 | 6 | 2 A46474 | FC epsilon RIb - A |
| 16 | 28.9 | 7 | 2 S08606 | hypothetical prote |
| 17 | 28.9 | 7 | 2 S42407 | gramicidin S synth |
| 18 | 28.9 | 7 | 2 PT0520 | T-cell receptor be |
| 19 | 28.9 | 9 | 2 PT0238 | Ig heavy chain CRD |
| 20 | 26.7 | 4 | 2 I38888 | COI Inton 16 prot |
| 21 | 26.7 | 4 | 2 A35779 | neuropeptide Antho |
| 22 | 26.7 | 4 | 2 PT0712 | T-cell receptor be |
| 23 | 26.7 | 5 | 2 S70154 | URF2 protein - Xan |
| 24 | 26.7 | 7 | 2 PC2370 | probable H+-transp |
| 25 | 26.7 | 7 | 2 PN0649 | alpha-dextrin endo |
| 26 | 26.7 | 7 | 2 S29735 | polynophosphate--glu |
| 27 | 26.7 | 8 | 2 XGH0EU | urine glycopeptide |
| 28 | 26.7 | 8 | 2 T14906 | hypothetical prote |
| 29 | 26.7 | 8 | 2 B27867 | homeotic protein U |

ALIGNMENTS

| | | | | | | |
|----|----|------|---|---|--------|---------------------|
| 30 | 12 | 26.7 | 8 | 2 | H41978 | CALLIFMRamide 8 - |
| 31 | 12 | 26.7 | 8 | 2 | A38887 | T-cell receptor ga |
| 32 | 12 | 26.7 | 9 | 2 | T31612 | hypothetical prote |
| 33 | 12 | 26.7 | 9 | 2 | JN0027 | [Phe-6]-mosact - s |
| 34 | 12 | 26.7 | 9 | 2 | S36850 | Ig heavy chain V r |
| 35 | 12 | 26.7 | 9 | 2 | PD0027 | pev-trachykinin - p |
| 36 | 11 | 24.4 | 4 | 2 | J01273 | neuropeptide Antho |
| 37 | 11 | 24.4 | 5 | 2 | JN0860 | peptidyl-dipeptida |
| 38 | 11 | 24.4 | 5 | 2 | I40698 | biotin B - Citroba |
| 39 | 11 | 24.4 | 5 | 2 | B37325 | pap fibribial regul |
| 40 | 11 | 24.4 | 6 | 2 | B34835 | dnaa protein - pse |
| 41 | 11 | 24.4 | 7 | 2 | B44787 | callifmramide 11 |
| 42 | 11 | 24.4 | 7 | 2 | I48086 | DNA topoisomerase |
| 43 | 11 | 24.4 | 8 | 2 | E60588 | sperm-activating p |
| 44 | 11 | 24.4 | 8 | 2 | G60588 | sperm-activating p |
| 45 | 11 | 24.4 | 9 | 1 | AKQIM | locustamyoinhibiti |

RESULT 1
S07205 litorin 2-Glu - Australian tree frog (Litoria aurea)
C:Species: Litoria aurea
C:Date: 12-Feb-1993 #sequence-revision 12-Mar-1993 #text-change 18-Aug-2000
C:Accession: S07205
R:Anastasi, A.; Montecucchi, P.; Angelucci, F.; Erspamer, V.; Endean, R.
Experientia 33, 1289, 1977
A:Title: Glu(OMe)(2)-litorin, the second bombesin-like peptide occurring in methanol
A:Reference number: S07205; MUID:78003546
A:Accession: S07205
A:Molecule type: protein
A:Residues: 1-9 <NA>
C:Superfamily: gastrin-releasing peptide
C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:9/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 37.8% Score 17; DB 2; Length 9;
Best Local Similarity 40.0% Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 lshf1 8
: 11;
DB 5 VGHFM 9

RESULT 2
S07204 litorin I - Australian tree frog (Litoria aurea)
C:Species: Litoria aurea
C:Date: 12-Feb-1993 #sequence-revision 12-Mar-1993 #text-change 18-Aug-2000
C:Accession: S07204
R:Anastasi, A.; Erspamer, V.; Endean, R.
Experientia 31, 510-511, 1975
A:Title: Aminoacid composition and sequence of litorin, a bombesin-like nonapeptide f
A:Reference number: S07204; MUID:75187011
A:Accession: S07204
A:Molecule type: protein
A:Residues: 1-9 <NA>
C:Superfamily: gastrin-releasing peptide
C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:9/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 37.8% Score 17; DB 2; Length 9;
Best Local Similarity 40.0% Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 4 lshf1 8

Db 5 VGHFM 9

RESULT 3

S07241
Iltorin - Rohde's leaf frog
C:Species: Phyllomedusa rohdei (Rohde's leaf frog)
C:Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000
C:Accession: S07241
R:Barra, D.; Falconieri Erspamer, G.; Simmaco, M.; Bossa, F.; Melchiorri, P.; Erspamer, F.B.S. Lett. 182, 53-56, 1985
A:Title: Rohdei-iltorin: a new peptide from the skin of Phyllomedusa rohdei.
A:Reference number: S07241; MUID:85127560
A:Accession: S07241
A:Molecule type: protein
A:Residues: 1-9 <BAR>
C:Superfamily: gastrin-releasing peptide
C:Keywords: amidated carboxyl end; blocked amino end; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:9/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 35.6%; Score 16; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0;

OY 6 hfl 8
||:
Db 7 HFM 9

RESULT 4

D48186
ARPAase R1 subunit - wood tobacco (fragment)
C:Species: Nicotiana sylvestris (wood tobacco)
C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 23-Feb-1997
C:Accession: D48186
R:De Paeppe, R.; Forchioni, A.; Chetrit, P.; Vedel, F.
Proc. Natl. Acad. Sci. U.S.A. 90, 5934-5938, 1993
A:Title: Specific mitochondrial proteins in pollen: presence of an additional ATP synthase
A:Reference number: A48186; MUID:93317598
A:Accession: D48186
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9
A:Experimental source: pollen
A:Note: sequence extracted from NCBI backbone (NCBIP:134871)

Query Match 35.6%; Score 16; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0;

OY 2 vdlshf 7
|||:
Db 3 VDLAPY 8

RESULT 5

PC4131
Hypothetical protein 8 [imported] - Pseudomonas aeruginosa (fragment)
C:Species: Pseudomonas aeruginosa
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: PC4131
R:Kawasaki, S.; Arai, H.; Igarashi, Y.; Kodama, T.
Gene 167, 87-91, 1995
A:Title: Sequencing and characterization of the downstream region of the genes encoding Y for biosynthesis of heme d1.
A:Reference number: JC4552; MUID:96144254
A:Accession: PC4131
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-8 <RAW>
A:Cross-references: DDBJ:D50473; NID:q1217594
A:Note: this ORF is not annotated in GenBank entry PSENIRC, release 113.0

Query Match 33.3%; Score 15; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0;

OY 3 dlsfl 8
|||:
Db 3 DLSRL 8

RESULT 6

JN0026
sperm-activating peptide SAP-b - sea urchin (Clypeaster japonicus)
N:Alternate names: [His-6]-mosact
C:Species: Clypeaster japonicus
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 18-Aug-2000
C:Accession: JN0026; B60973
R:Suzuki, N.; Kurita, M.; Yoshino, K.; Kajima, H.; Nomura, K.; Yamaguchi, M.
Zool. Sci. 4, 649-656, 1987
A:Title: Purification and structure of mosact and its derivatives from the egg jelly
A:Reference number: JN0025
A:Accession: JN0026
A:Molecule type: protein
A:Residues: 1-9 <SUZ>
R:Itakao, T.; Yoshino, K.; Suzuki, N.; Shimonishi, Y.
Biomed. Environ. Mass Spectrom. 19, 705-712, 1990
A:Title: Analysis of post-translational modifications of proteins by accurate mass measurement
A:Reference number: A60973; MUID:91167743
A:Accession: B60973
A:Molecule type: protein
A:Residues: 1-9 <TAK>
C:Comment: SAP-b (mosact), one of several sperm activating peptides located in egg jelly
C:Comment: Forms with and without the bromohistidine moiety were purified separately.
C:Superfamily: unassigned animal peptides
C:Keywords: bromine
F:6/Modified site: bromohistidine (His) (partial) #status experimental

Query Match 33.3%; Score 15; DB 2; Length 9;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 dlsfl 8
|||:
Db 3 DSAHLI 8

RESULT 7

A58728
Serratwettin W2 - Serratia marcescens
C:Species: Serratia marcescens
C:Date: 10-Feb-1998 #sequence_revision 12-Feb-1998 #text_change 12-Feb-1998
C:Accession: A58728
R:Matsuyama, T.; Kaneda, K.; Nakagawa, Y.; Isa, K.; Hara-Hotta, H.; Yano, I.
J. Bacteriol. 174, 1769-1776, 1992
A:Title: A novel extracellular cyclic lipopeptide which promotes flagellum-dependent
A:Reference number: A58728; MUID:92193260
A:Accession: A58728
A:Status: unencoded polypeptide
A:Molecule type: protein
A:Residues: 1-5 <MAT>
A:Experimental source: strain NS 25
C:Comment: A surfactant lipopeptide promoting flagellum-independent surface translocation
C:Keywords: blocked amino end; blocked carboxyl end; D-amino acid; lipoprotein; unenc
F:1/Modified site: D-leucine (Leu) #status experimental
F:4/Modified site: D-phenylalanine (Phe) #status experimental
F:1-5/Cross-link: 3-hydroxydecanoyl amino end, ester carboxyl end (Leu-11e) #status e

Query Match 31.1%; Score 14; DB 4; Length 5;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 lshfl 8
| | |
| | |
Db 1 LSTFL 5

RESULT 8
S20446
elastase - Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 24-Jul-1997
C:Accession: S20446
R:Kessler, E.; Saffin, M.; Peretz, M.; Birstein, Y.
FEBS Lett. 299, 291-293, 1992
A:Title: Identification of cleavage sites involved in proteolytic processing of Pseudom
A:Reference number: S20446; MUID:92183956
A:Accession: S20446
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <RES>

Query Match 31.1%; Score 14; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 avd1 4
| | |
| | |
Db 1 AADL 4

RESULT 9
S78024
ribosomal protein Yml21, mitochondrial - yeast (Saccharomyces cerevisiae) (fragment)
C:Species: Saccharomyces cerevisiae
C:Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 14-Nov-1997
C:Accession: S78024
R:Kitakawa, M.; Graack, H.R.; Grohmann, L.; Goldschmidt-Reisin, S.; Herfurth, E.; Wittma
Eur. J. Biochem. 245, 449-456, 1997
A:Title: Identification and characterization of the genes for mitochondrial ribosomal pr
A:Reference number: S78018; MUID:97296414
A:Accession: S78024
A:Molecule type: protein
A:Residues: 1-7 <KIT>
C:Genetics:
A:Genome: nuclear
C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 31.1%; Score 14; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 lshfl 9
| | |
| | |
Db 2 LXMLK 7

RESULT 10
A42057
fibroblast growth factor receptor 1, secreted - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
C:Accession: A42057
R:Werner, S.; Duan, D.S.R.; de Vries, C.; Peters, K.G.; Johnson, D.E.; Williams, L.T.
Mol. Cell. Biol. 12, 82-88, 1992
A:Title: Differential splicing in the extracellular region of fibroblast growth factor r
A:Reference number: A42057; MUID:92107200
A:Accession: A42057
A>Status: preliminary

A:Molecule type: DNA
A:Residues: 1-8 <MER>
A:Cross-references: GB:M80363
C:Keywords: growth factor receptor

Query Match 31.1%; Score 14; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 lshfl 8
| | |
| | |
Db 3 LTSFL 7

RESULT 11
S66296
Na⁺-transporting ATP synthase (EC 3.6.1.-) chain c - Acetobacterium woodii (fragment)
N:Alternate names: ATPase chain c
C:Species: Acetobacterium woodii
C:Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 07-May-1999
C:Accession: S66296
R:Reidlinger, J.; Mueller, V.
Eur. J. Biochem. 223, 275-283, 1994
A:Title: Purification of ATP synthase from Acetobacterium woodii and identification a
A:Reference number: S45648; MUID:94307271
A:Accession: S66296
A:Molecule type: protein
A:Residues: 1-8 <RES>
A:Experimental source: DSM 1030
C:Keywords: hydrolase

Query Match 31.1%; Score 14; DB 2; Length 8;
Best Local Similarity 28.6%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 dlsflk 9
| | |
| | |
Db 2 EILDFIK 8

RESULT 12
B39841
dextranucrase (EC 2.4.1.5) - Streptococcus sobrinus (fragment)
C:Species: Streptococcus sobrinus
C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 23-Jun-1993
C:Accession: B39841
R:Mooser, G.; Hefta, S.A.; Paxton, R.J.; Shively, J.E.; Lee, T.D.
J. Biol. Chem. 266, 8916-8922, 1991
A:Title: Isolation and sequence of an active-site peptide containing a catalytic aspa
A:Reference number: A39841; MUID:91224988
A:Accession: B39841
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <MOO>
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 31.1%; Score 14; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 avd 3
| | |
| | |
Db 7 AVD 9

RESULT 13
A39841
sucrose 3-glucosyltransferase (EC 2.4.1.-) - Streptococcus sobrinus (fragment)
C:Species: Streptococcus sobrinus
C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 21-Mar-1996

Search completed: July 3, 2002, 10:33:24
Job time: 178 sec

C:Accession: A39841
R:Mosser, G.; Hetta, S.A.; Paxton, R.J.; Shively, J.E.; Lee, T.D.
J. Biol. Chem. 266, 8916-8922, 1991
A:Title: Isolation and sequence of an active-site peptide containing a catalytic aspartate
A:Reference number: A39841; MUID:91224988
A:Accession: A39841
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <MOO>
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 31.1%; Score 14; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 avd 3
|||
Db 7 AVD 9

RESULT 14
C57444
neuropeptide Grb-AST B3 - two-spotted cricket
C:Species: Gryllus bimaculatus (two-spotted cricket)
C:Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C:Accession: C57444
R:Lorenz, M.W.; Kellner, R.; Hofmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995
A:Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cricket
A:Reference number: A57444; MUID:95403341
A:Accession: C57444
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <LOK>

Query Match 31.1%; Score 14; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 dls 5
|||
Db 4 DLS 6

RESULT 15
A46474
Fc epsilon RIIB - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1995
C:Accession: A46474
R:Richards, M.L.; Katz, D.H.; Liu, F.T.
J. Immunol. 147, 1067-1074, 1991
A:Title: Complete genomic sequence of the murine low affinity Fc receptor for IgE. Demonstration of a family of related genes
A:Reference number: A46474; MUID:91318149
A:Accession: A46474
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-6 <RIC>
A:Experimental source: BALB C, splenic B cells
A>Note: sequence extracted from NCBI backbone (NCBIP:45428)

Query Match 28.9%; Score 13; DB 2; Length 6;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 valsh 6
: | |
Db 1 MDTHH 5

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